



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Regents of the University of Minnesota
- (ii) TITLE OF THE INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merchant & Gould P.C.
 - (B) STREET: P.O. Box 2903
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402-0903
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/308,830
 - (B) FILING DATE: 04-AUG-1999
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US97/22228
 - (B) FILING DATE: 05-DEC-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/032,930
 - (B) FILING DATE: 06-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Skoog, Mark T
 - (B) REGISTRATION NUMBER: 40,178
 - (C) REFERENCE/DOCKET NUMBER: 600.346USWO
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-332-5300
 - (B) TELEFAX: 612-332-9081
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCATCACGGG TGGATTCTTG AACAGGTG

29

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATCACGCC CCCCGTCGAC GATAAAATAG TTGCTAAGCT ACAAGCT

47

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAATAA ATAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
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TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCATCACGGG TGGATCCTTG AAACAGGTGC A	31
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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 828...1580
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATCACGCA	TCACTCATGT	TTGACAGCTT	ATCATCGATA	AGCTTACTTT	TCGAATCAGG	60
TCTATCCTTG	AAACAGGTGC	AACATAGATT	AGGGCATGGA	GATTTACCAG	ACAACTATGA	120
ACGTATATAC	TCACATCACG	CAATCGGCAA	TTGATGACAT	TGGAACATAA	TTCAATCAAT	180
TTGTTACTAA	CAAGCAACTA	GATTGACAAC	TAATTCTCAA	CAAACGTTAA	TTTAACAACA	240
TTCAAGTAAC	TCCCACCAGC	TCCATCAATG	CTTACCGTAA	GTAATCATAA	CTTACTAAAA	300
CCTTGTTACA	TCAAGGTTTT	TTCTTTTTGT	CTTGTTTCATG	AGTTACCATA	ACTTTCTATA	360
TTATTGACAA	CTAAATTGAC	AACTCTTCAA	TTATTTTTCT	GTCTACTCAA	AGTTTTCTTC	420
ATTTGATATA	GTCTAATTCC	ACCATCACTT	CTTCCACTCT	CTCTACCGTC	ACAACTTCAT	480
CATCTCTCAC	TTTTTCGTGT	GGTAACACAT	AATCAAAATAT	CTTTCCGTTT	TTACGCACTA	540
TCGCTACTGT	GTCACCTAAA	ATATACCCCT	TATCAATCGC	TTCTTTAAAC	TCATCTATAT	600
ATAACATATT	TCATCCTCCT	ACCTATCTAT	TCGTAAAAAG	ATAAAAATAA	CTATTGTTTT	660
TTTTGTATT	TTATAATAAA	ATTATTAATA	TAAGTTAATG	TTTTTTAAAA	ATATACAATT	720
TTATTCTATT	TATAGTTAGC	TATTTTTTCA	TTGTTAGTAA	TATTGGTGAA	TTGTAATAAC	780
CTTTTAAAT	CTAGAGGAGA	ACCCAGATAT	AAAATGGAGG	AATATTA ATG	GAA AAC	836
				Met Glu Asn		
				1		
AAT AAA AAA	GTA TTG AAG	AAA ATG GTA	TTT TTT GTT	TTA GTG ACA	TTT	884
Asn Lys Lys	Val Leu Lys	Lys Lys Met	Val Phe Phe	Val Leu Val	Thr Phe	
5	10		15			
CTT GGA CTA	ACA ATC TCG	CAA GAG GTA	TTT GCT CAA	CAA GAC CCC	GAT	932
Leu Gly Leu	Thr Ile Ser	Gln Glu Val	Phe Ala Gln	Gln Gln Asp	Pro Asp	
20	25	30	35			
CCA AGC CAA	CTT CAC AGA	TCT AGT TTA	GTT AAA AAC	CTT CAA AAT	ATA	980
Pro Ser Gln	Leu His Arg	Ser Ser Leu	Val Lys Asn	Leu Gln Asn	Ile	
	40	45	50			
TAT TTT CTT	TAT GAG GGT	GAC CCT GTT	ACT CAC GAG	AAT GTG AAA	TCT	1028
Tyr Phe Leu	Tyr Glu Gly	Asp Pro Val	Thr His Glu	Asn Val Lys	Ser	
	55	60	65			
GTT GAT CAA	CTT TTA TCT	CAC CAT TTA	ATA TAT AAT	GTT TCA GGG	CCA	1076
Val Asp Gln	Leu Leu Ser	His His Leu	Ile Tyr Asn	Val Ser Gly	Pro	
70	75	80				
AAT TAT GAT	AAA TTA AAA	ACT GAA CTT	AAG AAC CAA	GAG ATG GCA	ACT	1124

Asn	Tyr	Asp	Lys	Leu	Lys	Thr	Glu	Leu	Lys	Asn	Gln	Glu	Met	Ala	Thr		
85						90					95						
TTA	TTT	AAG	GAT	AAA	AAC	GTT	GAT	ATT	TAT	GGT	GTA	GAA	TAT	TAC	CAT	1172	
Leu	Phe	Lys	Asp	Lys	Asn	Val	Asp	Ile	Tyr	Gly	Val	Glu	Tyr	Tyr	His		
100					105					110					115		
CTC	TGT	TAT	TTA	TGT	GAA	AAT	GCA	GAA	AGG	AGT	GCA	TGT	ATC	TAC	GGA	1220	
Leu	Cys	Tyr	Leu	Cys	Glu	Asn	Ala	Glu	Arg	Ser	Ala	Cys	Ile	Tyr	Gly		
				120					125					130			
GGG	GTA	ACA	AAT	CAT	GAA	GGG	AAT	CAT	TTA	GAA	ATT	CCT	AAA	AAG	ATA	1268	
Gly	Val	Thr	Asn	His	Glu	Gly	Asn	His	Leu	Glu	Ile	Pro	Lys	Lys	Ile		
			135					140					145				
GTC	GTT	AAA	GTA	TCA	ATC	GAT	GGT	ATC	CAA	AGC	CTA	TCA	TTT	GAT	ATT	1316	
Val	Val	Lys	Val	Ser	Ile	Asp	Gly	Ile	Gln	Ser	Leu	Ser	Phe	Asp	Ile		
		150					155					160					
GAA	ACA	AAT	AAA	AAA	ATG	GTA	ACT	GCT	CAA	GAA	TTA	GAC	TAT	AAA	GTT	1364	
Glu	Thr	Asn	Lys	Lys	Met	Val	Thr	Ala	Gln	Glu	Leu	Asp	Tyr	Lys	Val		
	165					170					175						
AGA	AAA	TAT	CTT	ACA	GAT	AAT	AAG	CAA	CTA	TAT	ACT	AAT	GGA	CCT	TCT	1412	
Arg	Lys	Tyr	Leu	Thr	Asp	Asn	Lys	Gln	Leu	Tyr	Thr	Asn	Gly	Pro	Ser		
180					185					190					195		
AAA	TAT	GAA	ACT	GGA	TAT	ATA	AAG	TTC	ATA	CCT	AAG	AAT	AAA	GAA	AGT	1460	
Lys	Tyr	Glu	Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Pro	Lys	Asn	Lys	Glu	Ser		
				200					205					210			
TTT	TGG	TTT	GAT	TTT	TTC	CCT	GAA	CCA	GAA	TTT	ACT	CAA	TCT	AAA	TAT	1508	
Phe	Trp	Phe	Asp	Phe	Phe	Pro	Glu	Pro	Glu	Phe	Thr	Gln	Ser	Lys	Tyr		
			215					220					225				
CTT	ATG	ATA	TAT	AAA	GAT	AAT	GAA	ACG	CTT	GAC	TCA	AAC	ACA	AGC	CAA	1556	
Leu	Met	Ile	Tyr	Lys	Asp	Asn	Glu	Thr	Leu	Asp	Ser	Asn	Thr	Ser	Gln		
		230					235				240						
ATT	GAA	GTC	TAC	CTA	ACA	ACC	AAG	TAAC	TTTTT	TTG	CTTTT	GGCAA	CCTT	ACCTAC		1610	
Ile	Glu	Val	Tyr	Leu	Thr	Thr	Lys										
	245					250											
TGCTGGATTT	AGAAATTTTA	TTGCAATTCT	TTTATTAATG	TAAAAACCGC	TCATTTGATG											1670	
AGCGGTTTTG	TCTTATCTAA	AGGAGCTTTA	CCTCCTAATG	CTGCAAAATT	TTAAATGTTG											1730	
GATTTTTGTA	TTTGTCCTATT	GTATTTGATG	GGTAATCCCA	TTTTTCGACA	GACATCGTCG											1790	
TGCCACCTCT	AACACCAAAA	TCATAGACAG	GAGCTTG TAG	CTTAGCAACT	ATTTTATCGT											1850	
C																1851	

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Asn	Asn	Lys	Lys	Val	Leu	Lys	Lys	Met	Val	Phe	Phe	Val	Leu
1				5				10						15	
Val	Thr	Phe	Leu	Gly	Leu	Thr	Ile	Ser	Gln	Glu	Val	Phe	Ala	Gln	Gln
			20					25					30		
Asp	Pro	Asp	Pro	Ser	Gln	Leu	His	Arg	Ser	Ser	Leu	Val	Lys	Asn	Leu
		35					40					45			
Gln	Asn	Ile	Tyr	Phe	Leu	Tyr	Glu	Gly	Asp	Pro	Val	Thr	His	Glu	Asn
	50					55					60				
Val	Lys	Ser	Val	Asp	Gln	Leu	Leu	Ser	His	His	Leu	Ile	Tyr	Asn	Val
65					70					75					80
Ser	Gly	Pro	Asn	Tyr	Asp	Lys	Leu	Lys	Thr	Glu	Leu	Lys	Asn	Gln	Glu
			85						90					95	
Met	Ala	Thr	Leu	Phe	Lys	Asp	Lys	Asn	Val	Asp	Ile	Tyr	Gly	Val	Glu
			100					105						110	
Tyr	Tyr	His	Leu	Cys	Tyr	Leu	Cys	Glu	Asn	Ala	Glu	Arg	Ser	Ala	Cys
		115				120						125			
Ile	Tyr	Gly	Gly	Val	Thr	Asn	His	Glu	Gly	Asn	His	Leu	Glu	Ile	Pro
	130					135					140				
Lys	Lys	Ile	Val	Val	Lys	Val	Ser	Ile	Asp	Gly	Ile	Gln	Ser	Leu	Ser
145					150					155					160
Phe	Asp	Ile	Glu	Thr	Asn	Lys	Lys	Met	Val	Thr	Ala	Gln	Glu	Leu	Asp
			165						170					175	
Tyr	Lys	Val	Arg	Lys	Tyr	Leu	Thr	Asp	Asn	Lys	Gln	Leu	Tyr	Thr	Asn
			180					185					190		
Gly	Pro	Ser	Lys	Tyr	Glu	Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Pro	Lys	Asn
		195					200					205			
Lys	Glu	Ser	Phe	Trp	Phe	Asp	Phe	Phe	Pro	Glu	Pro	Glu	Phe	Thr	Gln
	210					215					220				
Ser	Lys	Tyr	Leu	Met	Ile	Tyr	Lys	Asp	Asn	Glu	Thr	Leu	Asp	Ser	Asn
225					230					235					240
Thr	Ser	Gln	Ile	Glu	Val	Tyr	Leu	Thr	Thr	Lys					
			245						250						